



Microbe (Effect of Spaceflight on Microbial Gene Expression and Virulence in *S. typhimurium*, *P. aeruginosa*, *C. albicans*)

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Objective:

- Assess the effects of spaceflight on gene expression for 3 microbes: *S. typhimurium*, *P. aeruginosa*, and *C. albicans* by comparing spaceflight results with ground and modeled microgravity results.
- Assess the effects of spaceflight on the virulence potential of 3 microbes: *S. typhimurium*, *P. aeruginosa*, and *C. albicans* by comparing spaceflight results with ground and modeled microgravity results.



S. typhimurium



P. aeruginosa



C. albicans

Relevance/Impact:

- These microbes were chosen because they are well studied and either have been, or have the potential to be, isolated from the ISS, Space Shuttle, Mir, or their crew. This study is essential in determining microbial risks and options for mitigation.

Development Approach & Outcome:

- Cultures were flown in BioServe Group Activation Packs (GAPs) on STS -115 (12A). Microbe was a sortie.
- Upon return, flight samples were used for microarray studies to assess gene expression and in a mouse LD-50 study at KSC to assess changes in virulence potential.
- Following flight, microbes exhibited enhanced virulence in a rodent infection model.**
- Results suggest genetic targets to provide novel therapeutic options to decrease infections risk during spaceflight or on the Earth.**
- See Publication, PNAS, 9/2007

ISS Resource Requirements

Accommodation (carrier)	Middeck
Upmass (kg) (w/o packing factor)	12.29
Volume (m³) (w/o packing factor)	0.02
Power (kw) (peak)	0.0
Crew Time (hrs) (installation/operations)	2.0
Launch/Increment	12A/Increment 13

Project Life Cycle Schedule

Milestones	CT	Safety	FRR	Launch	Ops	Return	Final Report
Actual/ Baseline	5/11/06	2/10/06	7/15/06	9/9/06	Sortie	9/21/06	Return + 12m